XIV MEDECOS
&
XIII AEET meeting

Human driven scenarios for evolutionary and ecological changes

Abstract book

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EXCELENCIA SEVERO OCHOA

UNIVERSIDAD DE SEVILLA

Session 02: Historical biogeography of Mediterranean lineages

S.02-1-Invited Lecture

Parametric approaches for inferring the biogeographic history of Mediterranean lineages

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The Mediterranean region, with its mixture of small plates, age-old and young ocean basins, and changing paleoclimate history represents a challenge for biogeographic methods. Parsimony approaches based on area cladograms were for many years the only option available for inferring the biogeographic history of Mediterranean lineages. The recent development of parametric methods based on probabilistic models of range evolution has widened the range of questions that can be addressed with phylogenetic and spatial data. Unlike parsimony, these methods allow integration of time and additional sources of evidence, such as species' ecology, the fossil record, or Earth history. Here, I review these approaches and current challenges, with an emphasis on Mediterranean studies. Maximum-likelihood methods like Dispersal-Extinction-Cladogenesis (DEC) provide detailed reconstructions of the history of lineages, including numerous types of biogeographic processes (dispersal, extinction, speciation), at the expense of computational efficiency - though recent methodological extensions offer new promise. Bayesian biogeographic methods allow joint estimation of phylogenies, divergence times, and ancestral ranges given molecular and geographic data. Based on a simpler biogeographic model, the use of MCMC techniques and a Bayesian hierarchical approach to account for taxon-specific differences make these methods powerful to test hypotheses in macroevolution and ecology using datasets of multiple lineages. New research has focused on relaxing the time homogeneity of the process, allowing dispersal rates to vary over time, and on modelling extinction. Finally, other approaches use machine-learning techniques to increase the realism of biogeographic models, but they often include many parameters and model testing/fitting can be difficult.

S.02-2-Oral

A biogeography inquiry to decipher the origin of carob populations (Ceratonia siliqua, Leguminosae)

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Despite its economic importance, the origin and long-term history of carob tree (Ceratonia siliqua L.) are still under debate. Since De Candolle, the wildness of Mediterranean carob populations has been questioned on the basis of paleo-botanical, archeological and philological evidence but, unfortunately, the scarce studies on the ecology and genetic diversity of wild populations have not thrown much light on this topic. The extremely low cold-stress tolerance of carob plants constituted the main argument against a long-term persistence of natural populations throughout Pleistocene in the Mediterranean. Under this scenario, the current carob Mediterranean range would be explained by human dissemination from Western Asia. However, a global phylogeographic study covering the entire distribution of carob is still lacking. We sequenced nuclear and plastid regions from both natural and cultivated populations covering the whole current distribution range of carob to explore its phylogeography based on coalescent methods and divergence time estimations. Here we report the first molecular evidence on the origin of Ceratonia siliqua and we try to set the hypothetical events that shaped the historical biogeography of this tertiary relict lineage.